

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 01:32:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777245.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1777245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777245_1.fastq.gz SRR1777245_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 01:32:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,074,390
Mapped reads	10,668,342 / 96.33%
Unmapped reads	406,048 / 3.67%
Mapped paired reads	10,668,342 / 96.33%
Mapped reads, first in pair	5,357,842 / 48.38%
Mapped reads, second in pair	5,310,500 / 47.95%
Mapped reads, both in pair	10,575,200 / 95.49%
Mapped reads, singletons	93,142 / 0.84%
Secondary alignments	0
Supplementary alignments	430,182 / 3.88%
Read min/max/mean length	30 / 101 / 102.51
Duplicated reads (estimated)	1,945,496 / 17.57%
Duplication rate	15.4%
Clipped reads	6,970,472 / 62.94%

2.2. ACGT Content

Number/percentage of A's	256,384,820 / 28.07%
Number/percentage of C's	175,669,971 / 19.24%
Number/percentage of T's	277,534,587 / 30.39%
Number/percentage of G's	203,665,003 / 22.3%
Number/percentage of N's	17,111 / 0%

GC Percentage	41.54%
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2.3. Coverage

Mean	0.2952
Standard Deviation	2.4915

2.4. Mapping Quality

Mean Mapping Quality	51.49
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2.5. Insert size

Mean	247,486.82
Standard Deviation	4,856,583.68
P25/Median/P75	91 / 128 / 177

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	5,974,119
Insertions	93,289
Mapped reads with at least one insertion	0.86%
Deletions	257,111
Mapped reads with at least one deletion	2.37%
Homopolymer indels	48.24%

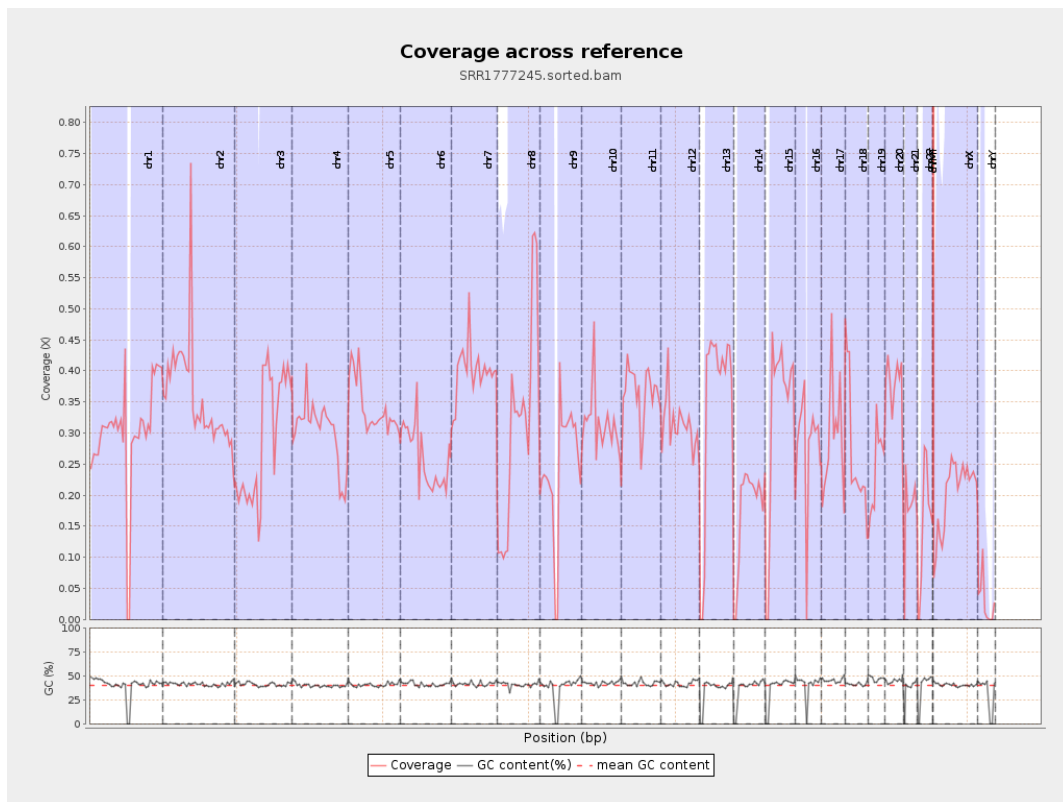
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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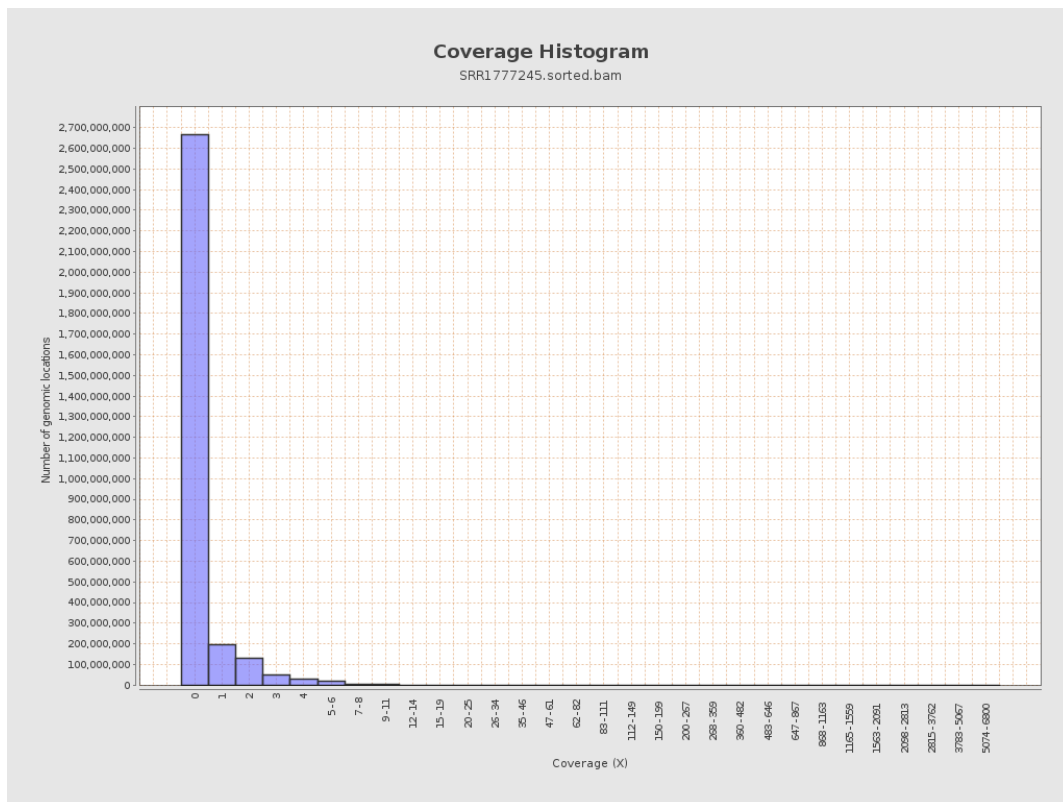
		bases	coverage	deviation
chr1	249250621	75053596	0.3011	3.6211
chr2	243199373	87237861	0.3587	2.7944
chr3	198022430	57351752	0.2896	0.9285
chr4	191154276	57967147	0.3032	1.2123
chr5	180915260	61637774	0.3407	1.0197
chr6	171115067	44218832	0.2584	4.8627
chr7	159138663	63421381	0.3985	3.1853
chr8	146364022	46256153	0.316	3.9012
chr9	141213431	34816016	0.2465	3.1002
chr10	135534747	42611826	0.3144	2.2254
chr11	135006516	49121037	0.3638	2.0411
chr12	133851895	41920705	0.3132	1.2723
chr13	115169878	40295051	0.3499	1.0269
chr14	107349540	19117263	0.1781	0.8506
chr15	102531392	33710071	0.3288	1.0034
chr16	90354753	24999613	0.2767	1.391
chr17	81195210	23462556	0.289	1.2354
chr18	78077248	20757886	0.2659	3.7828
chr19	59128983	14338549	0.2425	2.462
chr20	63025520	24035132	0.3814	1.1097
chr21	48129895	8646130	0.1796	0.9156
chr22	51304566	7863515	0.1533	0.6731
chrMT	16571	1846507	111.43	56.1744
chrX	155270560	31287591	0.2015	1.0215

chrY	59373566	1760987	0.0297	1.0266
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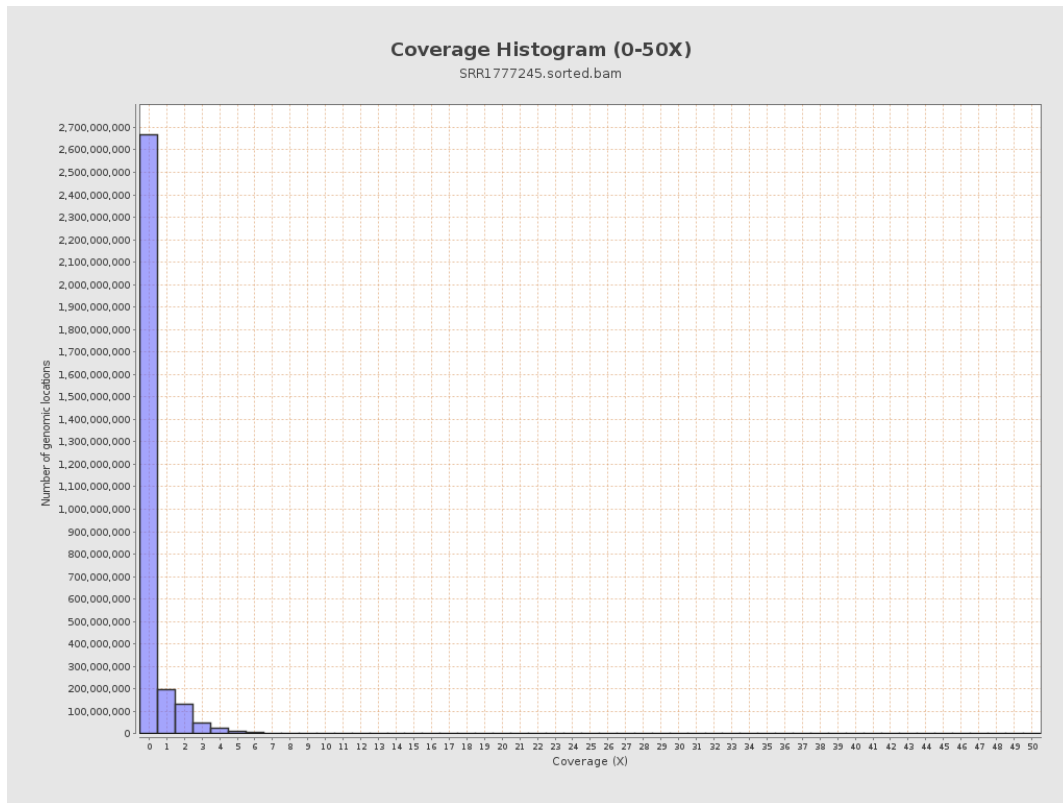
3. Results : Coverage across reference



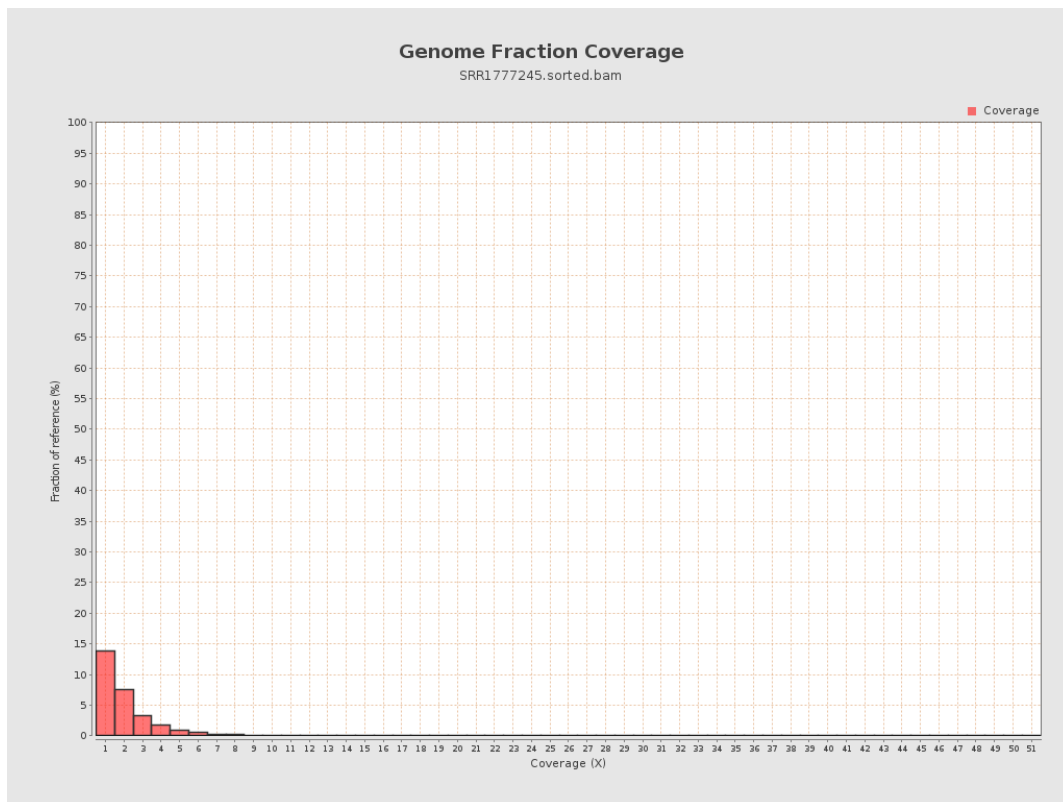
4. Results : Coverage Histogram



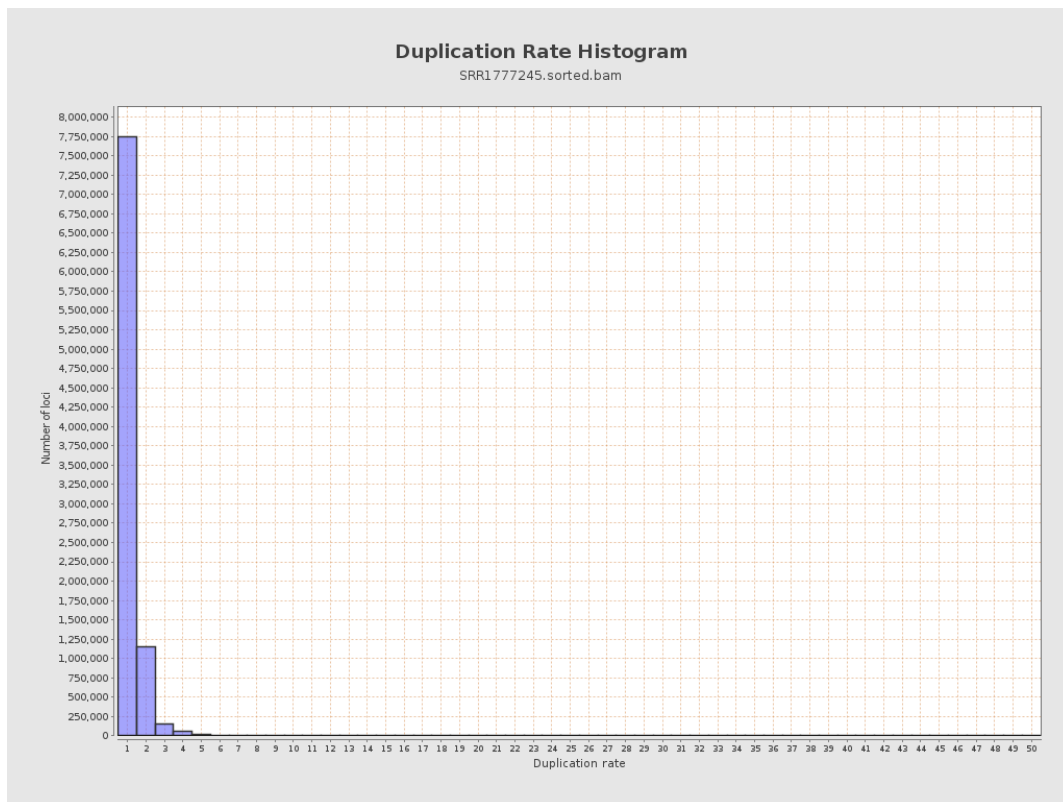
5. Results : Coverage Histogram (0-50X)



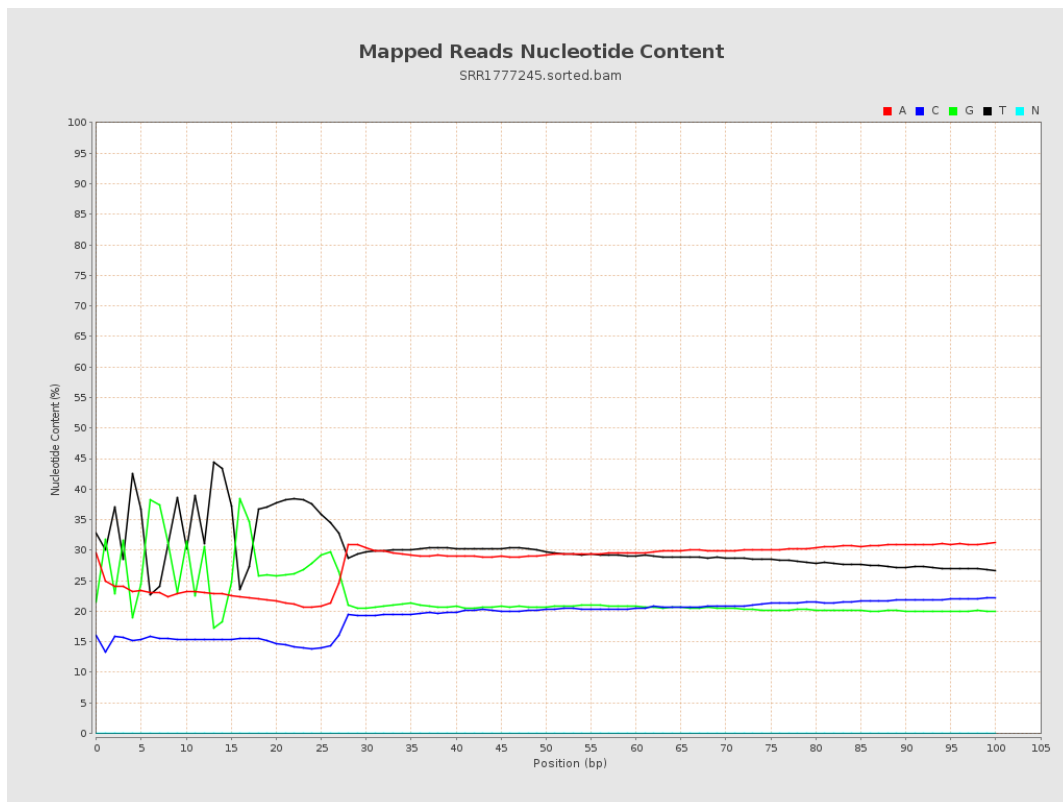
6. Results : Genome Fraction Coverage



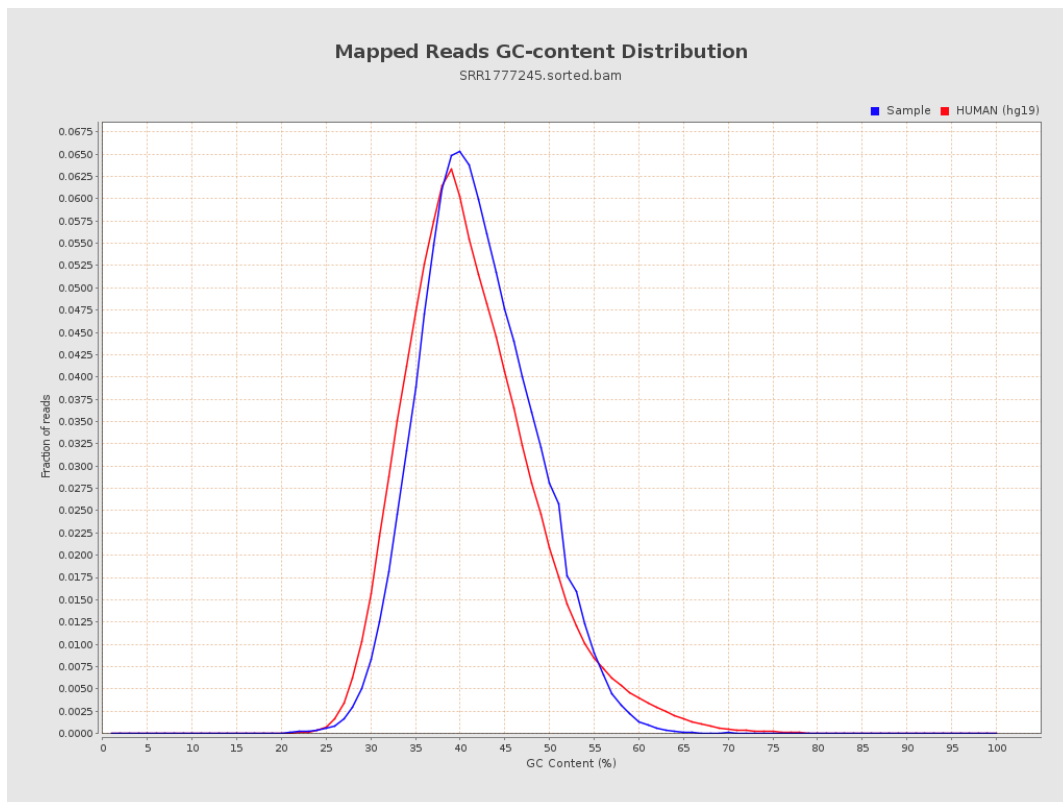
7. Results : Duplication Rate Histogram



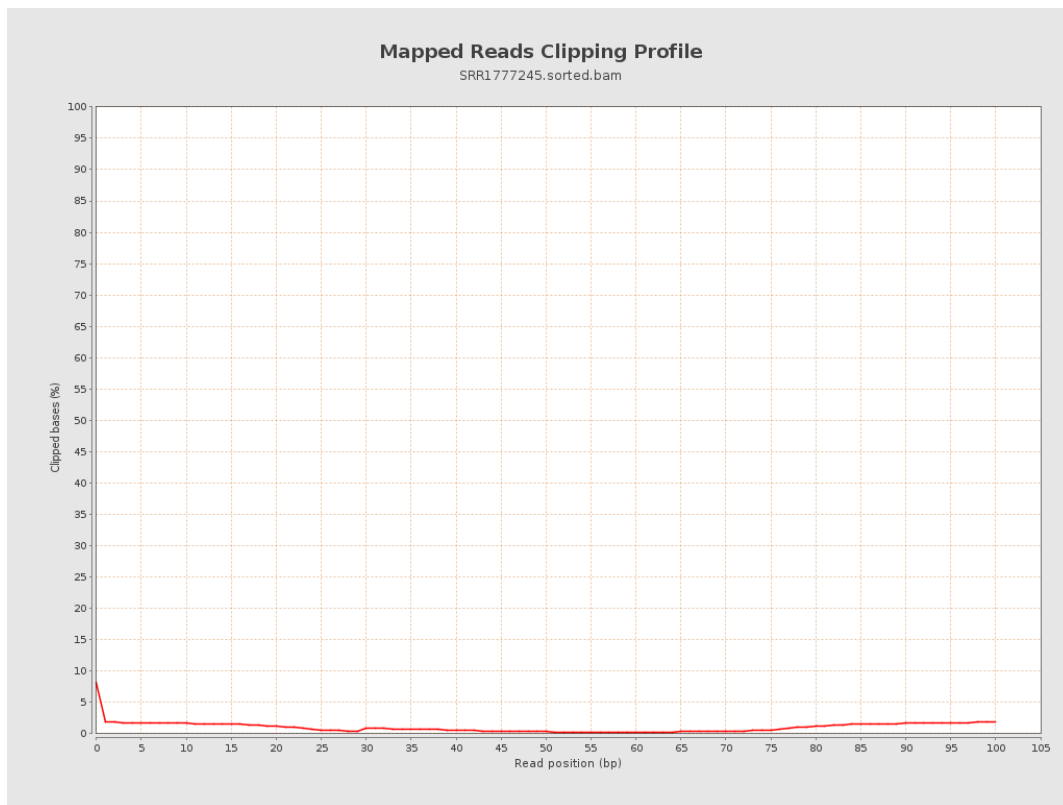
8. Results : Mapped Reads Nucleotide Content



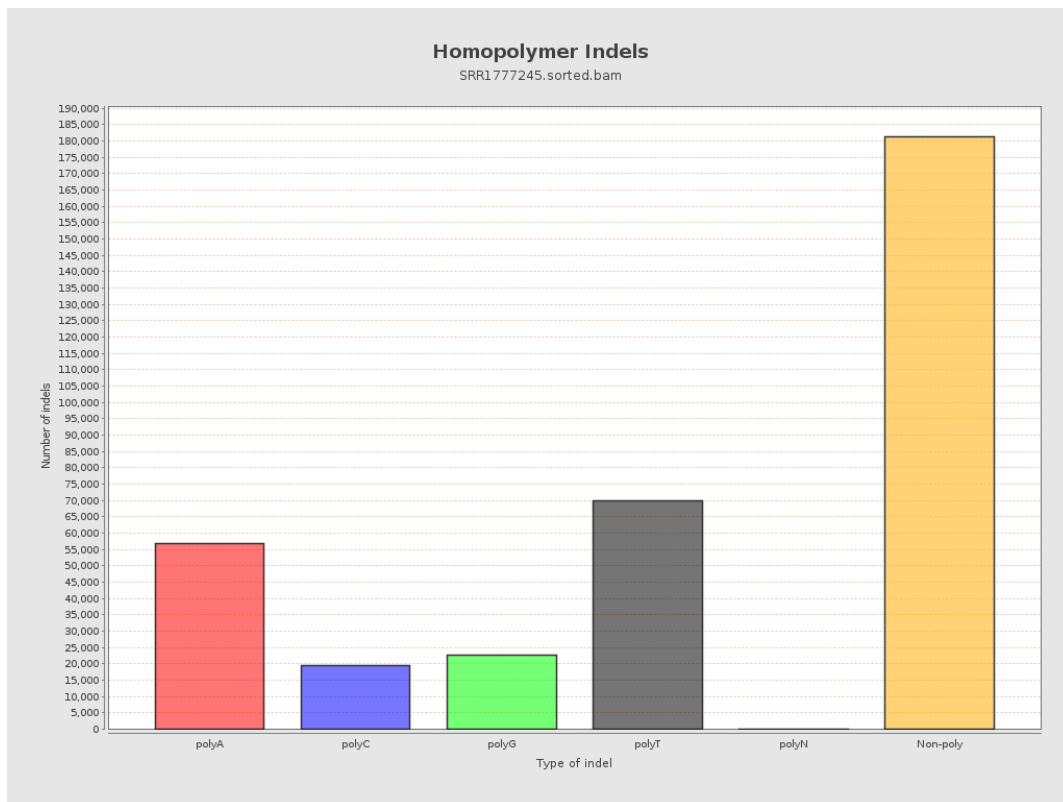
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



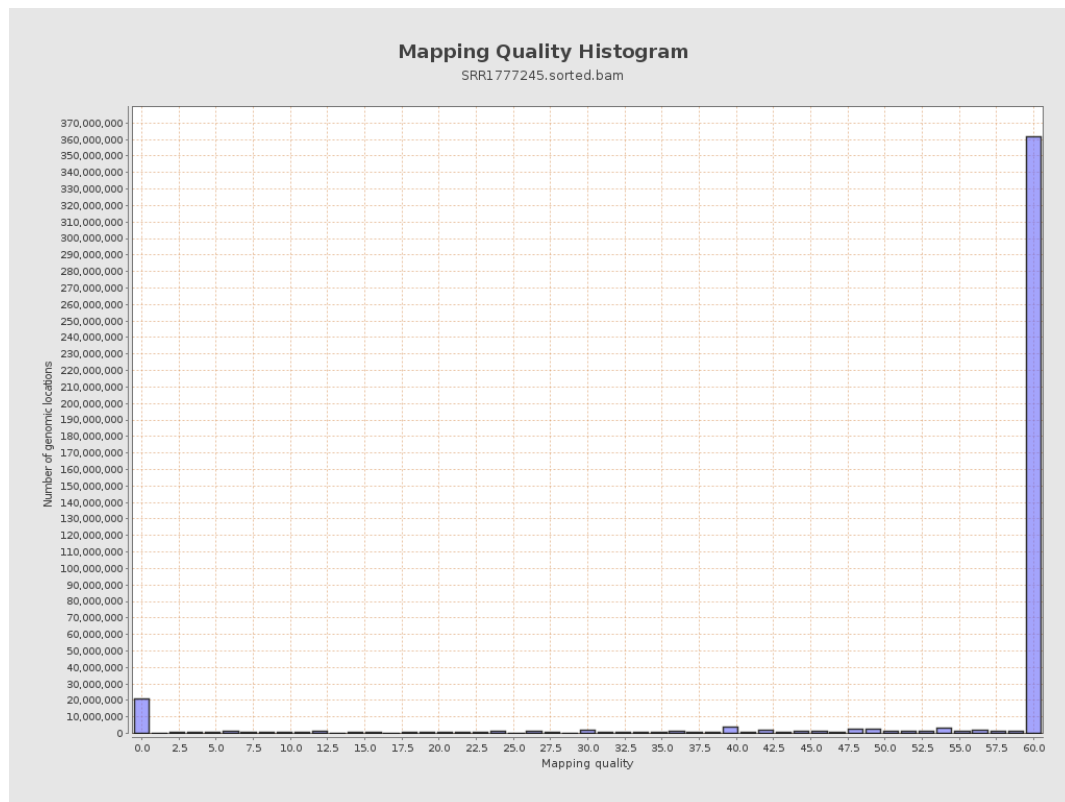
11. Results : Homopolymer Indels



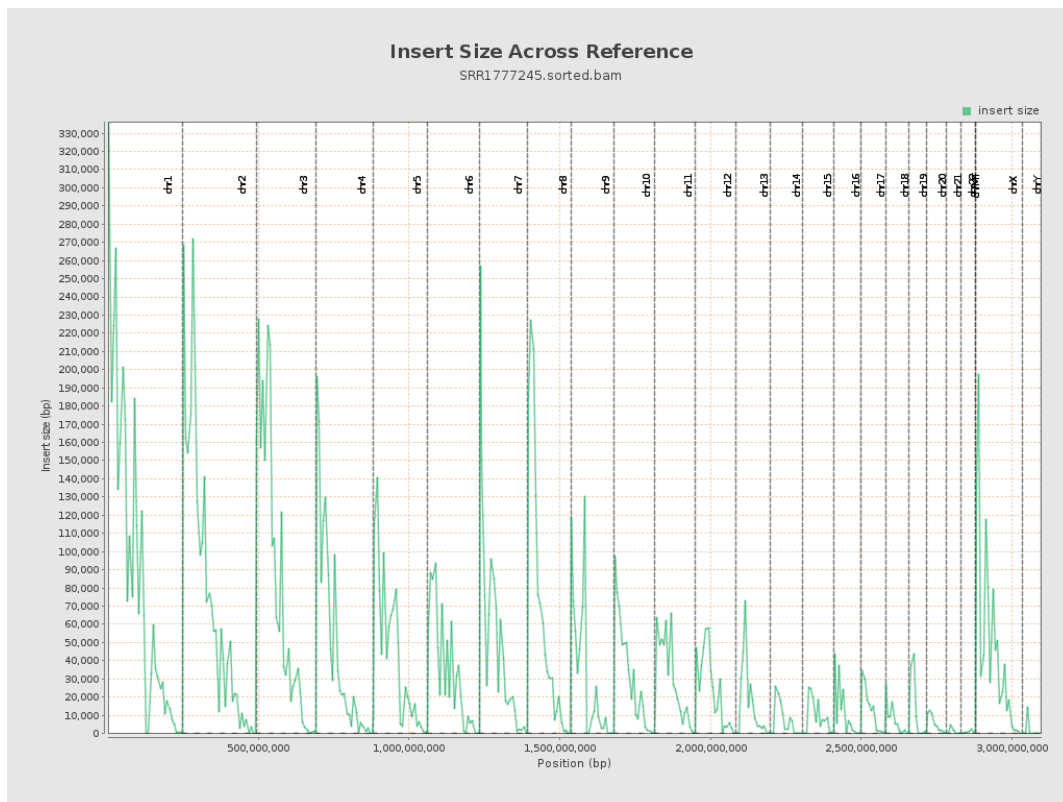
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

